RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/806,232C_
Source: _1Fw/6_
Date Processed by STIC: _6/30/05_

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RAW SEQUENCE LISTING   DATE: 06/30/2005
PATENT APPLICATION: US/09/806,232C TIME: 10:17:39

Input Set : A:\1241.18 Sequence Listing.txt
Output Set: N:\CRF4\06302005\I806232C.raw

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 3 <110> APPLICANT: Seiki Motoharu
 5 <120> TITLE OF INVENTION: DNA CODING FOR NOVEL POLIPEPTIDE
 7 <130> FILE REFERENCE: 1241.18
 9 <140> CURRENT APPLICATION NUMBER: 09/806,232C
10 <141> CURRENT FILING DATE: 2001-03-28
12 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05349
13 <151> PRIOR FILING DATE: 1999-09-29
15 <150> PRIOR APPLICATION NUMBER: JP10-276258
16 <151> PRIOR FILING DATE: 1998-09-29
18 <150> PRIOR APPLICATION NUMBER: JP10-291505
19 <151> PRIOR FILING DATE: 1998-09-29
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 587
27 <212> TYPE: PRT
28 <213> ORGANISM: Mouse
30 <400> SEQUENCE: 1
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32  1               5                  10                  15
34 Pro Arg Pro Gly Pro Gly Leu Pro Pro Leu Leu Leu Val Leu Ala Leu
35              20                  25                  30
37 Ala Ala His Gly Gly Cys Ala Ala Pro Ala Pro Arg Ala Glu Asp Leu
38              35                  40                  45
40 Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr Leu Pro Pro Ala
41          50                  55                  60
43 Asp Pro Ala Ser Gly Gln Leu Gln Thr Gln Glu Glu Leu Ser Lys Ala
44  65                  70                  75                  80
46 Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Thr Thr Gly Ile Leu
47              85                  90                  95
49 Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg Cys Ser Leu Pro
50              100                 105                 110
52 Asp Leu Pro Pro Gly Ala Gln Ser Arg Arg Lys Arg Gln Thr Pro Pro
53          115                 120                 125
55 Pro Thr Lys Trp Ser Lys Arg Asn Leu Ser Trp Arg Val Arg Thr Phe
56      130                 135                 140
58 Pro Arg Asp Ser Pro Leu Gly Arg Asp Thr Val Arg Ala Leu Met Tyr
59 145                 150                 155                 160
61 Tyr Ala Leu Lys Val Trp Ser Asp Ile Thr Pro Leu Asn Phe His Glu
62              165                 170                 175
64 Val Ala Gly Asn Ala Ala Asp Ile Gln Ile Asp Phe Ser Lys Ala Asp
65              180                 185                 190
67 His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly Thr Val Ala His
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68          195                200                205
70 Ala Phe Phe Pro Gly Asp His His Thr Ala Gly Asp Thr His Phe Asp
71     210                215                220
73 Asp Asp Glu Pro Trp Thr Phe Arg Ser Ser Asp Ala His Gly Met Asp
74 225       '         230                235                240
76 Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala Ile Gly Leu Ser
77               245                250                255
79 His Val Ala Ala Pro Ser Ser Ile Met Gln Pro Tyr Tyr Gln Gly Pro
80               260                265                270
82 Val Gly Asp Pro Val Arg Tyr Gly Leu Pro Tyr Glu Asp Arg Val Arg
83          275                280                285
85 Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser Pro Thr Ala Gln
86     290                295                300
88 Leu Asp Thr Pro Glu Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro
89 305                310                315                320
91 Asn Asn Arg Ser Ser Thr Pro Pro Gln Lys Asp Val Pro His Arg Cys
92               325                330                335
94 Thr Ala His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe
95          340                345                350
97 Phe Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val
98          355                360                365
100 Ser Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu
101     370                375                380
103 His Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys
104 385                390                395                400
106 Ile Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn
107               405                410                415
109 Val Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro
110          420                425                430
112 Gly Gly Ile Asp Ala Val Phe Ser Trp Ala His Asn Asp Arg Thr Tyr
113          435                440                445
115 Phe Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg Arg
116     450                455                460
118 Met Asp Pro Gly Tyr Pro Ala Gln Gly Pro Leu Trp Arg Gly Val Pro
119 465                470                475                480
121 Ser Met Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe
122               485                490                495
124 Phe Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Ala
125          500                505                510
127 Ala Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly
128          515                520                525
130 Glu Pro Leu Ala Asp Ala Glu Asp Val Gly Pro Gly Pro Gln Gly Arg
131     530                535                540
133 Ser Gly Ala Gln Asp Gly Leu Ala Val Cys Ser Cys Thr Ser Asp Ala
134 545               550                555                560
136 His Arg Leu Ala Leu Pro Ser Leu Leu Leu Leu Thr Pro Leu Leu Trp
137               565                570                575
139 Gly Leu Trp Thr Ser Val Ser Ala Lys Ala Ser
140          580                585
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142 <210> SEQ ID NO: 2
143 <211> LENGTH: 606
144 <212> TYPE: PRT
145 <213> ORGANISM: Homo sapiens
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149   1               5                  10                  15
151 Gly Leu Ser Arg Leu Pro Leu Leu Pro Leu Pro Leu Leu Leu Leu Leu
152              20                  25                  30
154 Ala Leu Gly Thr Arg Gly Gly Cys Ala Ala Pro Glu Pro Ala Arg Arg
155              35                  40                  45
157 Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg Phe Gly Tyr
158      50                  55                  60
160 Leu Pro Pro Ala Asp Pro Thr Thr Gly Gln Leu Gln Thr Gln Glu Glu
161  65                  70                  75                  80
163 Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly Leu Glu Ala
164              85                  90                  95
166 Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys Thr Pro Arg
167             100                 105                 110
169 Cys Ser Leu Pro Asp Leu Pro Val Leu Thr Gln Ala Arg Arg Arg Arg
170             115                 120                 125
172 Gln Ala Pro Ala Pro Thr Lys Trp Asn Lys Arg Asn Leu Ser Trp Arg
173      130                 135                 140
175 Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly His Asp Thr Val Arg
176 145                 150                 155                 160
178 Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile Ala Pro Leu
179             165                 170                 175
181 Asn Phe His Glu Val Ala Gly Ser Thr Ala Asp Ile Gln Ile Asp Phe
182             180                 185                 190
184 Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly Pro Gly Gly
185             195                 200                 205
187 Thr Val Ala His Ala Phe Phe Pro Gly His His His Thr Ala Gly Asp
188      210                 215                 220
190 Thr His Phe Asp Asp Asp Glu Ala Trp Thr Phe Arg Ser Ser Asp Ala
191 225                 230                 235                 240
193 His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe Gly His Ala
194             245                 250                 255
196 Ile Gly Leu Ser His Val Ala Ala Ala His Ser Ile Met Arg Pro Tyr
197             260                 265                 270
199 Tyr Gln Gly Pro Val Gly Asp Pro Leu Arg Tyr Gly Leu Pro Tyr Glu
200             275                 280                 285
202 Asp Lys Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu Ser Val Ser
203      290                 295                 300
205 Pro Thr Ala Gln Pro Glu Glu Pro Pro Leu Leu Pro Glu Pro Pro Asp
206 305                 310                 315                 320
208 Asn Arg Ser Ser Ala Pro Pro Arg Lys Asp Val Pro His Arg Cys Ser
209             325                 330                 335
211 Thr His Phe Asp Ala Val Ala Gln Ile Arg Gly Glu Ala Phe Phe Phe
212             340                 345                 350
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214 Lys Gly Lys Tyr Phe Trp Arg Leu Thr Arg Asp Arg His Leu Val Ser
215         355                 360                 365
217 Leu Gln Pro Ala Gln Met His Arg Phe Trp Arg Gly Leu Pro Leu His
218     370                 375                 380
220 Leu Asp Ser Val Asp Ala Val Tyr Glu Arg Thr Ser Asp His Lys Ile
221 385                 390                 395                 400
223 Val Phe Phe Lys Gly Asp Arg Tyr Trp Val Phe Lys Asp Asn Asn Val
224                 405                 410                 415
226 Glu Glu Gly Tyr Pro Arg Pro Val Ser Asp Phe Ser Leu Pro Pro Gly
227                 420                 425                 430
229 Gly Ile Asp Ala Ala Phe Ser Trp Ala His Asn Asp Arg Thr Tyr Phe
230             435                 440                 445
232 Phe Lys Asp Gln Leu Tyr Trp Arg Tyr Asp Asp His Thr Arg His Met
233     450                 455                 460
235 Asp Pro Gly Tyr Pro Ala Gln Ser Pro Leu Trp Arg Gly Val Pro Ser
236 465                 470                 475                 480
238 Thr Leu Asp Asp Ala Met Arg Trp Ser Asp Gly Ala Ser Tyr Phe Phe
239                 485                 490                 495
241 Arg Gly Gln Glu Tyr Trp Lys Val Leu Asp Gly Glu Leu Glu Val Ala
242             500                 505                 510
244 Pro Gly Tyr Pro Gln Ser Thr Ala Arg Asp Trp Leu Val Cys Gly Asp
245             515                 520                 525
247 Ser Gln Ala Asp Gly Ser Val Ala Ala Gly Val Asp Ala Ala Glu Gly
248     530                 535                 540
250 Pro Arg Ala Pro Pro Gly Gln His Asp Gln Ser Arg Ser Glu Asp Gly
251 545                 550                 555                 560
253 Tyr Glu Val Cys Ser Cys Thr Ser Gly Ala Ser Ser Pro Pro Gly Ala
254             565                 570                 575
256 Pro Gly Pro Leu Val Ala Ala Thr Met Leu Leu Leu Leu Pro Pro Leu
257             580                 585                 590
259 Ser Pro Gly Ala Leu Trp Thr Ala Ala Gln Ala Leu Thr Leu
260         595                 600                 605
262 <210> SEQ ID NO: 3
263 <211> LENGTH: 3517
264 <212> TYPE: DNA
265 <213> ORGANISM: Mouse
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (86)..(1846)
271 <400> SEQUENCE: 3
272 ggcacgaggg cgcggagccg agcgaggcgc ggagctggct gctggcgggt gcggggaccc 60
274 tcgccacccg acctgggaga gcggg atg gga cgc cgc ccg cgg gga cct ggg 112
275                            Met Gly Arg Arg Pro Arg Gly Pro Gly
276                             1                 5
278 tcc ccc cgg gga cct ggc cct cca cgc ccc ggg ccg ggg ctg cca cca 160
279 Ser Pro Arg Gly Pro Gly Pro Pro Arg Pro Gly Pro Gly Leu Pro Pro
280 10                 15                 20                 25
282 ctg ctg ctt gta ctg gcg ctg gcg gcc cat ggg ggc tgc gca gcg ccc 208
283 Leu Leu Leu Val Leu Ala Leu Ala Ala His Gly Gly Cys Ala Ala Pro
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284                    30                  35                    40
286 gcg ccc cgc gcg gag gac ctc agc ctc ggg gtg gag tgg cta agc agg   256
287 Ala Pro Arg Ala Glu Asp Leu Ser Leu Gly Val Glu Trp Leu Ser Arg
288                    45                  50                    55
290 ttt ggc tac ctg ccg cct gca gat ccg gca tca ggg cag cta cag acc   304
291 Phe Gly Tyr Leu Pro Pro Ala Asp Pro Ala Ser Gly Gln Leu Gln Thr
292              60                  65                  70
294 cag gag gaa ctg tcc aaa gcg att act gcc atg cag cag ttt ggt ggt   352
295 Gln Glu Glu Leu Ser Lys Ala Ile Thr Ala Met Gln Gln Phe Gly Gly
296         75                  80                  85
298 ctg gag acc act ggc atc cta gat gag gcc act ctg gcc ctg atg aaa   400
299 Leu Glu Thr Thr Gly Ile Leu Asp Glu Ala Thr Leu Ala Leu Met Lys
300 90                  95                  100                   105
302 acc cct cga tgc tcc ctt ccg gac ctg ccc cct ggg gcc caa tcg aga   448
303 Thr Pro Arg Cys Ser Leu Pro Asp Leu Pro Pro Gly Ala Gln Ser Arg
304              110                 115                 120
306 agg aag cgg cag act cca ccc cca acc aaa tgg agc aag agg aac ctt   496
307 Arg Lys Arg Gln Thr Pro Pro Pro Thr Lys Trp Ser Lys Arg Asn Leu
308              125                 130                 135
310 tct tgg agg gtc cgg aca ttc cca cgg gac tca ccc ctg ggc cgg gat   544
311 Ser Trp Arg Val Arg Thr Phe Pro Arg Asp Ser Pro Leu Gly Arg Asp
312         140                 145                 150
314 act gtg cgt gca ctc atg tac tac gcc ctc aaa gtc tgg agt gac atc   592
315 Thr Val Arg Ala Leu Met Tyr Tyr Ala Leu Lys Val Trp Ser Asp Ile
316         155                 160                 165
318 aca ccc ttg aac ttc cac gag gta gcg ggc aac gcg gcg gac atc cag   640
319 Thr Pro Leu Asn Phe His Glu Val Ala Gly Asn Ala Ala Asp Ile Gln
320 170                 175                 180                   185
322 atc gac ttc tcc aag gcc gac cac aat gac ggc tac ccc ttc gat ggc   688
323 Ile Asp Phe Ser Lys Ala Asp His Asn Asp Gly Tyr Pro Phe Asp Gly
324              190                 195                 200
326 cct ggt ggc acg gtg gcc cac gca ttc ttc cct ggt gac cac cac acg   736
327 Pro Gly Gly Thr Val Ala His Ala Phe Phe Pro Gly Asp His His Thr
328              205                 210                 215
330 gca ggg gac acc cac ttt gat gac gat gag cca tgg acc ttc cgt tcc   784
331 Ala Gly Asp Thr His Phe Asp Asp Asp Glu Pro Trp Thr Phe Arg Ser
332         220                 225                 230
334 tca gat gcc cac ggg atg gac ctg ttt gca gtg gcc gtc cat gag ttt   832
335 Ser Asp Ala His Gly Met Asp Leu Phe Ala Val Ala Val His Glu Phe
336         235                 240                 245
338 ggt cat gcc att ggt ctg agc cat gtt gcc gcc cca agc tcc atc atg   880
339 Gly His Ala Ile Gly Leu Ser His Val Ala Ala Pro Ser Ser Ile Met
340 250                 255                 260                   265
342 caa ccg tac tac cag ggc ccc gtg ggt gac ccc gta cgc tat gga ctt   928
343 Gln Pro Tyr Tyr Gln Gly Pro Val Gly Asp Pro Val Arg Tyr Gly Leu
344              270                 275                 280
346 ccc tat gag gac agg gtg cgt gtc tgg cag ttg tac ggt gtg cgg gaa   976
347 Pro Tyr Glu Asp Arg Val Arg Val Trp Gln Leu Tyr Gly Val Arg Glu
348         285                 290                 295
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VERIFICATION SUMMARY   DATE: 06/30/2005
PATENT APPLICATION: **US/09/806,232C**   TIME: 10:17:40

Input Set : **A:\1241.18 Sequence Listing.txt**
Output Set: **N:\CRF4\06302005\I806232C.raw**

L:1368 M:112 C: (48) String data converted to lower case,